

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 16, 2006, 15:33:20 ; Search time 47 Seconds  
(without alignments)  
51.013 Million cell updates/sec

Title: US-10-600-389A-3

Perfect score: 145

Sequence: 1 MKSFITRNKTALATVAATGTAIGAYYYY 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgm2\_6/ptodata/1/1aa/5 COMB.pep.\*
- 2: /cgm2\_6/ptodata/1/1aa/6 COMB.pep.\*
- 3: /cgm2\_6/ptodata/1/1aa/H COMB.pep.\*
- 4: /cgm2\_6/ptodata/1/1aa/PCUS COMB.pep.\*
- 5: /cgm2\_6/ptodata/1/1aa/RE COMB.pep.\*
- 6: /cgm2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	29	2	US-10-165-873D-3
2	145	100.0	41	2	US-08-789-333F-27
3	145	100.0	41	2	US-09-169-015-37
4	145	100.0	41	2	US-09-133-944-26
5	145	100.0	41	2	US-09-208-827-28
6	145	100.0	41	2	US-08-787-738B-27
7	145	100.0	41	2	US-09-157-748-29
8	145	100.0	41	2	US-08-800-170-80
9	145	100.0	41	2	US-09-626-581D-40
10	145	100.0	41	2	US-09-415-765B-40
11	145	100.0	41	2	US-09-626-580C-40
12	145	100.0	41	2	US-09-749-959-36
13	145	100.0	41	2	US-10-043-074-28
14	145	100.0	41	2	US-09-285-912A-89
15	145	100.0	41	2	US-09-578-030-31
16	145	100.0	41	2	US-09-916-940-27
17	145	100.0	41	2	US-09-419-381-74
18	145	100.0	41	2	US-10-142-662-41
19	145	100.0	41	2	US-10-086-550-27
20	145	100.0	41	2	US-09-062-330-23
21	145	100.0	41	2	US-10-226-877A-32
22	145	100.0	41	2	US-10-177-725-156
23	74	51.0	137	2	US-09-248-796A-26561
24	52	35.9	347	2	US-09-097-889-14
25	52	35.9	347	2	US-09-098-079-14
26	51	35.2	279	2	US-09-248-796A-17246
27	51	35.2	422	2	US-09-198-452A-772

28	51	35.2	835	2	US-09-438-185A-728	Sequence 728, App
29	50.5	34.8	739	2	US-09-503-922-1	Sequence 1, Appli
30	50	34.5	140	2	US-09-330-914A-9	Sequence 9, Appli
31	50	34.5	602	2	US-09-569-037-6	Sequence 6, Appli
32	49	33.8	201	2	US-09-605-703B-488	Sequence 488, App
33	49	33.8	238	2	US-09-605-703B-486	Sequence 486, App
34	49	33.8	348	2	US-09-931-401B-2	Sequence 2, Appli
35	49	33.8	501	2	US-09-530-851-2	Sequence 2, Appli
36	49	33.8	777	2	US-09-543-681A-4272	Sequence 4272, Ap
37	48	33.1	230	2	US-09-134-000C-4631	Sequence 4631, Ap
38	48	33.1	244	2	US-09-252-991A-22373	Sequence 22373, A
39	48	33.1	507	2	US-09-949-016-11300	Sequence 11300, A
40	48	33.1	977	2	US-08-335-844A-22	Sequence 22, Appli
41	48	33.1	977	2	US-09-129-366-22	Sequence 22, Appli
42	47	32.4	140	2	US-09-252-991A-21038	Sequence 21038, A
43	47	32.4	198	2	US-09-107-532A-6808	Sequence 6808, Ap
44	47	32.4	275	2	US-09-107-532A-7236	Sequence 7236, Ap
45	47	32.4	345	2	US-09-328-352-6565	Sequence 6565, Ap

## ALIGNMENTS

RESULT 1  
US-10-165-873D-3  
; Sequence 3, Application US/10165873D  
; Patent No. 6878524  
; GENERAL INFORMATION:  
; APPLICANT: Peng, Gang  
; APPLICANT: Hopper, James E.  
; APPLICANT: Vyshkina, Tamara E.  
; TITLE OF INVENTION: Reagents And Methods For Detection And Characterization Of  
; TITLE OF INVENTION: Protein-Protein Interactions, Nuclear Export And Localization  
; TITLE OF INVENTION: Sequences And Inducible Gal4p-Mediated Gene Expression In Ye  
; FILE REFERENCE: 02-133  
; CURRENT APPLICATION NUMBER: US/10/165,873D  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/296983  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 3  
; LENGTH: 29  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: mitochondria outer membrane signal anchor  
US-10-165-873D-3

Query Match 100.0%; Score 145; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2e-15;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKSFITRNKTALATVAATGTAIGAYYYY 29  
Db 1 MKSFITRNKTALATVAATGTAIGAYYYY 29

RESULT 2  
US-08-789-333F-27  
; Sequence 27, Application US/08789333F  
; Patent No. 6153380  
; GENERAL INFORMATION:  
; APPLICANT: No. 6153380an, Garry P  
; APPLICANT: Rothenberg, S. M.  
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR  
; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES  
; FILE REFERENCE: A642601DJBMSDSS  
; CURRENT APPLICATION NUMBER: US/08/789,333F  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: 08/589,108  
; PRIOR FILING DATE: 1996-01-23  
; PRIOR APPLICATION NUMBER: 08/589,911

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OM protein - protein search, using sw model

Run on: March 16, 2006, 15:36:21 ; Search time 195 Seconds  
(without alignments)  
36.052 Million cell updates/sec

Title: US-10-600-389A-1

Perfect score: 86

Sequence: 1 MGCTVSTQTIGDESDP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	16	6	ABP97556 Amino aci
2	86	100.0	16	6	ABP97553 N-myristo
3	86	100.0	16	8	ADH51063 Myristoyl
4	86	100.0	17	6	ABP97558 Amino aci
5	86	100.0	66	2	AAW69646 N-termina
6	86	100.0	66	2	AAW69647 N-termina
7	86	100.0	66	2	AAW69644 N-termina
8	86	100.0	66	2	AAW69639 N-termina
9	86	100.0	66	2	AAW69645 N-termina
10	86	100.0	66	2	AAW74443 Human Gal
11	86	100.0	66	2	AAW74442 Human Gal
12	86	100.0	66	2	AAW74440 Human Gal
13	86	100.0	66	2	AAW74435 Human Gal
14	86	100.0	66	2	AAW74441 Human Gal
15	86	100.0	66	3	AAW20745 GPAL amin
16	86	100.0	66	3	AAW20752 GPAL and
17	86	100.0	66	3	AAW20750 GPAL and
18	86	100.0	66	3	AAW20751 GPAL and
19	86	100.0	66	3	AAW20753 GPAL and
20	86	100.0	66	6	ABU10277 N-termina
21	86	100.0	66	6	ABU10284 N-termina
22	86	100.0	66	6	ABU10283 N-termina
23	86	100.0	66	6	ABU10285 N-termina
24	86	100.0	66	6	ABU10282 N-termina

25	86	100.0	86	ADI37116	Adi37116 Yeast cel
26	86	100.0	86	ADI37118	Adi37118 Yeast cel
27	86	100.0	86	ADI37115	Adi37115 Yeast cel
28	86	100.0	86	ADI37117	Adi37117 Yeast cel
29	86	100.0	86	ADI37110	Adi37110 Yeast cel
30	86	100.0	86	ADS15955	Adsi15955 Yeast GPA
31	86	100.0	86	ADS15961	Adsi15961 Yeast GPA
32	86	100.0	86	ADS15963	Adsi15963 Yeast GPA
33	86	100.0	86	ADS15960	Adsi15960 Yeast GPA
34	86	100.0	86	ADS15962	Adsi15962 Yeast GPA
35	86	100.0	472	2	AAW02220 Chimeric
36	86	100.0	472	2	AAW02222 Chimeric
37	86	100.0	472	2	AAW02224 Chimeric
38	86	100.0	472	2	AAW02217 Chimeric
39	86	100.0	472	2	AAW02225 Chimeric
40	86	100.0	472	2	AAW02218 Chimeric
41	86	100.0	472	2	AAW02223 Chimeric
42	86	100.0	472	2	AAW02219 Chimeric
43	86	100.0	472	2	AAW02221 Chimeric
44	86	100.0	472	8	ADS43591 Bacterial
45	86	100.0	892	2	AAW16314 Human thr
46	86	100.0	906	2	AAW16313 Yeast alp
47	80	93.0	16	6	ABP97554 Variant N
48	80	93.0	16	6	ADH51064 Myristoyl
49	71	82.6	478	2	AAW02226 Chimeric
50	49	57.0	457	8	ADH66746 Plant ful
51	48	55.8	1887	6	ABU20638 Protein e
52	44	51.2	99	2	AAW49658 Sequence
53	44	51.2	267	8	ADH70883 Plant ful
54	43	50.0	280	6	ABU45571 Protein e
55	43	50.0	315	8	ADH47247 Thermococ
56	42	48.8	27	5	AAU89413 Insulin/i
57	42	48.8	250	6	ABU48134 Protein e
58	42	48.8	296	8	ADH93313 Plant ful
59	42	48.8	314	4	AAW96250 Putative
60	42	48.8	314	6	ABU29263 Protein e
61	42	48.8	314	8	ADH43182 Bacterial
62	42	48.8	314	8	ADH18637 Bacterial
63	42	48.8	314	8	ADH41926 Bacterial
64	42	48.8	317	7	ADH88571 Enterococ
65	42	48.8	409	6	ABU31446 Protein e
66	42	48.8	458	4	AAU36166 Klebsiell
67	42	48.8	458	6	ABU31195 Protein e
68	42	48.8	474	7	ABO64180 Klebsiell
69	42	48.8	594	8	ADY25234 Plant ful
70	42	48.8	826	8	ADH71222 Human pro
71	42	48.8	826	8	ADH71270 Human pro
72	42	48.8	826	8	ADH71260 Human pro
73	42	48.8	826	8	ADH71278 Human pro
74	42	48.8	826	8	ADH71280 Human pro
75	42	48.8	832	8	ADH71224 Human pro
76	42	48.8	832	8	ADH71224 Human sof
77	42	48.8	2144	8	ADQ19484 Human sof
78	42	48.8	2333	8	ADH71274 Human pro
79	42	48.8	2733	4	AAU08680 Human FCT
80	42	48.8	2733	7	ADH32024 Human FCT
81	42	48.8	2733	8	ADH71250 Human pro
82	42	48.8	2733	8	ADH71254 Human pro
83	42	48.8	2733	8	ADH71240 Human pro
84	42	48.8	2733	8	ADH71246 Human pro
85	42	48.8	2733	8	ADH71258 Human pro
86	42	48.8	2802	5	ADH16953 Chicken N
87	41.5	48.3	413	5	ABP97264 Novel hum
88	41.5	48.3	413	5	ADH05991 Insulin/i
89	41	47.7	27	5	AAU89437 Propionib
90	41	47.7	79	4	AAU53330 Propionib
91	41	47.7	79	6	ABM49849 Human sig
92	41	47.7	146	6	ABO27187 Human sig
93	41	47.7	201	4	ABG18865 Novel hum
94	41	47.7	211	8	ADH87734 Plant ful
95	41	47.7	314	4	AAU35229 Enterococ
96	41	47.7	361	2	AAW42281 PGE2 rece
97	41	47.7	365	2	AAW42280 PGE2 rece